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<110> Liaw, Chen W. Chalmers, Derek T. Behan, Dominic P. Maciejewski-Lenior, Dominique Leonard, James N. Ortuno, Daniel Lin, I-Lin

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Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Ser Ala Ile Leu Pro Phe 65 70 75 80

Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe 85 90 95

Leu Cys Lys Leu Val His Val Met Ile Asp Ile Asn Leu Phe Val Ser 100 105 110

Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu 115 120 125

His Pro Ala Trp Ala Gln Asn His Arg Thr Met Ser Leu Ala Lys Arg 130 135 140

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Phe Ile Phe Trp Thr Thr Ile Ser Thr Thr Asn Gly Asp Thr Tyr Cys 165 170 175 Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn

Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile

Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile

Ala Ala Lys Ile His Arg Asn His Met Ile Lys Ser Ser Arg Pro Leu

Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro

Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu

Leu Asn Gly Lys Tyr Lys Ile Ile Leu Val Leu Ile Asn Pro Thr Ser

Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe

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Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser 50 55 60

Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe 65 70 75 80

Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val 85 90 95

Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn 100 105 110

Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe 115 120 125

Ile Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg 130 135 140

Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu 145 150 155 160

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n Val Phe As
n Leu Asp165 170 175

Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu 180 185 190

Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile 195 200 205

Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe 210 215 220

Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe 225 230 235 240

Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr 245 250 255

His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val 260 265 270

Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr 275 280 285

Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys 290 295 300

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Ile Met Leu Ser Leu Cys Cys Met Pro Phe Thr Ala Val Thr Leu Ile 90 85

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Cys Ile Ala Gly Pro Ser Leu Thr Gly Trp Thr Leu Val Glu Val Pro 170 165

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Arg Ala Tyr Val Val Thr Leu Val Val Ala Val Phe Phe Ala Pro Phe 195 200 205

Gly Val Met Leu Cys Ala Tyr Met Cys Ile Leu Asn Thr Val Arg Lys 210 215 220

Asn Ala Val Arg Val His Asn Gln Ser Asp Ser Leu Asp Leu Arg Gln 225 230 235 240

Leu Thr Arg Ala Gly Leu Arg Arg Leu Gln Arg Gln Gln Gln Val Ser 245 250 255

Val Asp Leu Ser Phe Lys Thr Lys Ala Phe Thr Thr Ile Leu Ile Leu 260 265 270

Phe Val Gly Phe Ser Leu Cys Trp Leu Pro His Ser Val Tyr Ser Leu 275 280 285

Leu Ser Val Phe Ser Gln Arg Phe Tyr Cys Gly Ser Ser Phe Tyr Ala 290 295 300

Thr Ser Thr Cys Val Leu Trp Phe Ser Tyr Leu Lys Ser Val Phe Asn 305 310 315 320

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Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly 50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu 65 70 75 80

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Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp 100 105 110

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Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile 305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile 325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser 340 345 350

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Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe 465 470 475 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly 485 490 495

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- Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys 565 570 575
- Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val 580 585 590
- Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val 595 600 605
- Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser 610 620
- Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr 625 630 635 640
- Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser 645 650 655
- Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala 660 665 670
- Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys 675 680 685
- Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala 690 695 700
- Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp 705 710 715 720
- Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys 725 730 735
- Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr 740 745 750

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<213> Homo sapiens

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Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val $35 \ \ \, 40 \ \ \, 45$

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg 50 55 60

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe 65 70 75 80

Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro 85 90 95

Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln 115 120 125

Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu 130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly 145 150 155 160

Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala 165 170 175

Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser 180 185 190

His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu

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<212> PRT

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Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser 225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln 245 250 255

Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe 260 265 270

Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His 275 280 285

Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala 290 295 300

Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe 305 310 315 320

His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile 325 330 335

Val Pro Tyr Ile Glu Val Ala Ser Leu Gly Val Thr Thr Phe Thr Leu 340 345 350

Cys Ala Leu Cys Ile Asp Arg Phe Arg Ala Ala Thr Asn Val Gln Met 355 360 365

Tyr Tyr Glu Met Ile Glu Asn Cys Ser Ser Thr Thr Ala Lys Leu Ala 370 375 380

Val Ile Trp Val Gly Ala Leu Leu Leu Ala Leu Pro Glu Val Val Leu 385 390 395 400

Arg Gln Leu Ser Lys Glu Asp Leu Gly Phe Ser Gly Arg Ala Pro Ala 405 410 415

Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr 420 425 430

Val Leu Ala Leu Thr Tyr Asp Ser Ala Arg Leu Trp Trp Tyr Phe Gly 440 435

Cys Tyr Phe Cys Leu Pro Thr Leu Phe Thr Ile Thr Cys Ser Leu Val 450 455

Thr Ala Arg Lys Ile Arg Lys Ala Glu Lys Ala Cys Thr Arg Gly Asn 470 465

Lys Arg Gln Ile Gln Leu Glu Ser Gln Met Asn Cys Thr Val Val Ala 490 485

Leu Thr Ile Leu Tyr Gly Phe Cys Ile Ile Pro Glu Asn Ile Cys Asn 505 500

Ile Val Thr Ala Tyr Met Ala Thr Gly Val Ser Gln Gln Thr Met Asp 515 520

Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Cys Val 535 540 530

Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe 555

Met Glu Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser 565 570

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Val Gly Thr His Cys 610

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<212> PRT

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<223> Novel Sequence

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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys 20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val

- Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu 50 55 60
- Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn 65 70 75 80
- Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu 85 90 95
- Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 100 105 110
- Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr 115 120 125
- Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln 130 135 140
- Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe 165 170 175
- Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser 180 185 190
- Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp 195 200 205
- Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val 210 215 220
- Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg 225 230 235 240
- Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser 245 250 255
- Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser 260 265 270

Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	Leu	Leu	Ile	Leu
		275		_			280					285			

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe 290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu 305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys 325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys 340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly 355 360

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<211> 403

<212> PRT

<213> Homo sapiens

<400> 14

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Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln 20 25 30

Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe 35 40 45

Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg 50 55 60

His Lys Ala Met Arg Thr Pro Thr Asn Tyr Tyr Leu Phe Ser Leu Ala 65 70 75 80

Val Ser Asp Leu Leu Val Leu Leu Val Gly Leu Pro Leu Glu Leu Tyr 85 90 95

Glu Met Trp His Asn Tyr Pro Phe Leu Leu Gly Val Gly Gly Cys Tyr 100 105 110

Phe Arg Thr Leu Leu Phe Glu Met Val Cys Leu Ala Ser Val Leu Asn 115 120 125

Val Thr Ala Leu Ser Val Glu Arg Tyr Val Ala Val His Pro Leu 130 135 140

Gln Ala Arg Ser Met Val Thr Arg Ala His Val Arg Arg Val Leu Gly 145 150 155 160

Ala Val Trp Gly Leu Ala Met Leu Cys Ser Leu Pro Asn Thr Ser Leu 165 170 175

His Gly Ile Arg Gln Leu His Val Pro Cys Arg Gly Pro Val Pro Asp 180 185 190

Ser Ala Val Cys Met Leu Val Arg Pro Arg Ala Leu Tyr Asn Met Val 195 200 205

Val Gln Thr Thr Ala Leu Leu Phe Phe Cys Leu Pro Met Ala Ile Met 210 215 220

Ser Val Leu Tyr Leu Leu Ile Gly Leu Arg Leu Arg Arg Glu Arg Leu 225 230 235 240

Leu Leu Met Gln Glu Ala Lys Gly Arg Gly Ser Ala Ala Ala Arg Ser 245 250 255

Arg Tyr Thr Cys Arg Leu Gln Gln His Asp Arg Gly Arg Arg Gln Val 260 265 270

Thr Lys Met Leu Phe Val Leu Val Val Val Phe Gly Ile Cys Trp Ala 275 280 285

Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr 290 295 300

Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile 305 310 315 320

Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met 325 330 335

Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala 340 345 350

Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg

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Val His Pro Leu Ala Gly Asn Asp Gly Pro Glu Ala Gln Glu Thr 385 390 395 400

Asp Pro Ser

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<210> 16 <211> 309 <212> PRT <213> Homo sapiens

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Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val 20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg 35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val 50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu 65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr 85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val 100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg 115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val 130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly 145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro 165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Phe Cys Ser Leu 180 185 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln 195 200 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu

210 215 220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg 225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg 245 250 255

Ala Ile Cys Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala 275 280 285

Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu 290 295 300

Cys Val Thr Leu Ala 305

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<211> 481

<212> PRT

<213> Homo sapiens

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His Arg Ala Glu Thr Gln Glu Gln Gln Ser Arg Ser Lys Arg Gly Thr 35 40 45

Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp 50 55 60

Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys 65 70 75 80

Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro 85 90 95

Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln 100 105 110

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr 115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly 130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr 145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp 165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile 180 185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe 195 200 205

Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu 210 215 220

Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg 225 230 235 240

Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp 245 250 255

Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Trp Gln Leu 265 270

Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met 275 280 285

Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr 290 295 300

Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu 305 310 315 320

Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg 325 330 335

Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln 340 345 350

Cys Glu Ser Gln Leu Asn Ser Thr Val Val Gly Leu Thr Val Val Tyr 355 360 365

Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr 370 375 380

Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile 385 390 395 400

Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu 405 410 415

Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys 420 425 430

Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala 435 440 445

Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr 450 455 460

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Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Asn Thr Ile Cys Tyr 50 60

Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Ser Ala Ile Leu Pro Phe 65 70 75 80

Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe 85 90 95

Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu 115 120 125

His Pro Ala Trp Ala Gln Asn His Arg Thr Met Ser Leu Ala Lys Arg 130 135 140

Val Met Thr Gly Leu Trp Ile Phe Thr Ile Val Leu Thr Leu Pro Asn 145 150 155 160

Phe Ile Phe Trp Thr Thr Ile Ser Thr Thr Asn Gly Asp Thr Tyr Cys 165 170 175

Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn 180 185 190

Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile 195 200 205

Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile 210 215 220

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Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro 245 250 255

Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu 260 265 270

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Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe 65 70 75 80

Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val 85 90 95

Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn 100 105 110

Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe 115 120 125

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Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu 85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp 100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln 115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe 130 135 140

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Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser 340 345 350

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Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala

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<211> 915

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 69

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- Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly 50 60
- Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu 65 70 75 80
- Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu 85 90 95
- Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$
- Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln 115 120 125
- Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe 130 135 140
- Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser 145 150 155 160
- Val Ser Ile Met Val Ala As
n Ile Leu Arg Leu Phe Gl
n Ile Pro Gl
n 165 $$170\$
- Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Tyr 180 185 190
- Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala 195 200 205
- Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu 210 215 220
- Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln 225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile 245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys 260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn 275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Lys Arg Ala Asp Gln 290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile 305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile 325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser 340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp 355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu 370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser 385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr \$405\$

Ala Met Ala His Ala Leu His His Met As
n Lys Asp Leu Cys Ala Asp 420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu 435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro $450 \ \ \, 460 \ \ \,$

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe

Equila
M
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interior interior
M
ine ine

Gln	Tyr	Gln	Thr	Thr 485	Asn	Thr	Ser	Asn	Pro 490	_	Tyr	Arg	Leu	Ile 495	Gly
Gln	Trp	Thr	Asp	Glu	Leu	Gln	Leu	Asn	Ile	Glu	Asp	Met	Gln	Trp	Gly

500 505 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys 515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr 530 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys 545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys 565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val 580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val 595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser 610 615 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr 625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser 645 650 655

Phe Arg His Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala 660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys 675 680 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala 690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp 705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr 740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val 755 760 765

Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe 770 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val 785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu 805 810 815

Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser 820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile 835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys 850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro 865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val 885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn 900 905 910

Leu Val Ile 915

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Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe

<210> 71

<211> 915

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 71

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Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly 50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu 65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile As
n Ser Asp Pro As
n Leu Leu 85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln 115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe 130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser 145 150 155 .

Val Ser Ile Met Val Ala As
n Ile Leu Arg Leu Phe Gl
n Ile Pro Gl
n 165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Tyr 180 185 190

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala 195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu 210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln 225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile 245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys 260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn 275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln 290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile 305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile 325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser 340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp 355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu 370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser 385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr \$405\$ \$410\$ \$415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp 420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu 435 440 445

Val 465	Met	Phe	Asn	Lys	Asn 470	Gly	Asp	Ala	Pro	Gly 475	Arg	Tyr	Asp	Ile	Phe 480
Gln	Tyr	Gln	Thr	Thr 485	Asn	Thr	Ser	Asn	Pro 490	Gly	Tyr	Arg	Leu	Ile 495	Gly
Gln	Trp	Thr	Asp 500	Glu	Leu	Gln	Leu	Asn 505	Ile	Glu	Asp	Met	Gln 510	Trp	Gly
Lys	Gly	Val 515	Arg	Glu	Ile	Pro	Ala 520	Ser	Val	Cys	Thr	Leu 525	Pro	Cys	Lys
Pro	Gly 530	Gln	Arg	Lys	Lys	Thr 535	Gln	Lys	Gly	Thr	Pro 540	Cys	Cys	Trp	Thr
Cys 545	Glu	Pro	Cys	Asp	Gly 550	Tyr	Gln	Tyr	Gln	Phe 555	Asp	Glu	Met	Thr	Cys 560
Gln	His	Cys	Pro	Tyr 565	Asp	Gln	Arg	Pro	Asn 570	Glu	Asn	Arg	Thr	Gly 575	Cys
Gln	Asp	Ile	Pro 580	Ile	Ile	Lys	Leu	Glu 585	Trp	His	Ser	Pro	Trp 590	Ala	Val
Ile	Pro	Val 595	Phe	Leu	Ala	Met	Leu 600	Gly	Ile	Ile	Ala	Thr 605	Ile	Phe	Val
Met	Ala 610	Thr	Phe	Ile	Arg	Tyr 615	Asn	Asp	Thr	Pro	Ile 620	Val	Arg	Ala	Ser
Gly 625	Arg	Glu	Leu	Ser	Tyr 630	Val	Leu	Leu	Thr	Gly 635	Ile	Phe	Leu	Cys	Tyr 640
Ile	Ile	Thr	Phe	Leu 645	Met	Ile	Ala	Lys	Pro 650	Asp	Val	Ala	Val	Cys 655	Ser
	-	_	Val 660			-		665		-			670		
Leu	Leu	Thr 675	Lys	Thr	Asn	Arg	Ile 680	Tyr	Arg	Ile	Phe	Glu 685	Gln	Gly	Lys

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala 690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp 705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr 740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val 755 760 765

Thr Cys Cys Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe 770 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val 785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu 805 810 815

Lys Leu Tyr Ile Gln Thr Thr Leu Thr Ile Ser Met Asn Leu Ser 820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile 835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys 850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro 865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val 885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn $900 \hspace{1.5cm} 905 \hspace{1.5cm} 910$

Leu Val Ile

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<220>

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<210> 73

⁹¹⁵

<211> <211> <212> PRT

<213> Unknown

<220>

<223> Novel Sequence

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Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp 35 40 45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly 50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu 65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu 85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp 100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln \$115\$ \$120\$ \$125\$

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe 130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser 145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
165 170 175

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala 195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu 210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln 225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gl
n Ser Val Arg Ile 245 $\,$ 250 $\,$ 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys 260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn 275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Lys Arg Ala Asp Gln 290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile 305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile 325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser 340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp 355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu 370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser 385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr 405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp 420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu 435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro

450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe 465 470 475 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly 485 490 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly 500 505 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys 515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr 530 535 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys 545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val 580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val 595 600

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser 610 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr 625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser 645 650 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala 660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys 675 680 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala 690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp 705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys 725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr 740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val 755 760 765

Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe 770 780

Asn Glu Ala Lys Pro Lys Gly Phe Thr Met Tyr Thr Thr Cys Ile Val 785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gl
n Ser Ala Glu 805 810 815

Lys Leu Tyr Ile Gln Thr Thr Leu Thr Ile Ser Met Asn Leu Ser 820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile $835 \\ 840 \\ 845$

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys 850 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro 865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val 885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn 900 905 910

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1320

attaagatet eteetgattt accagaeace atetatgtte tageeeteae etaegaeagt

gcgagactgt ggtggtattt tggctgttac ttttgtttgc ccacgctttt caccatcacc 1380 tgctctctag tgactgcgag gaaaatccgc aaagcagaga aagcctgtac ccgagggaat 1440 aaacggcaga ttcaactaga gagtcagatg aactgtacag tagtggcact gaccatttta 1500 tatggatttt gcattattcc tgaaaatatc tgcaacattg ttactgccta catggctaca 1560 ggggtttcac agcagacaat ggacctcctt aatatcatca qccagttcct tttqttcttt 1620 aagteetgtg teaccecagt ceteettte tgtetetgea aaccetteag tegggeette 1680 atggagtgct gctgctgttg ctgtgaggaa tgcattcaga agtcttcaac ggtgaccagt 1740 gatgacaatg acaacgagta caccacggaa ctcgaactct cgcctttcag taccatacgc 1800 cgtgaaatgt ccacttttgc ttctgtcgga actcattgct ga 1842

<210> 75

<211> 613

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 75

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Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro 20 25 30

Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val 35 40 45

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg 50 60

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe 65 70 75 80

Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro 85 90 95

Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro 100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln 115 120 125

Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu 130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly 145 150 155 160

Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala 165 170 175

Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser 180 185 190

His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu 195 200 205

Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser 210 215 220

Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser 225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln \$245\$ 250 255

Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe 260 265 270

Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His 275 280 285

Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala 290 295 300

Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe 305 310 315 320

His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile 325 330 335

Val Pro Tyr Ile Glu Val Ala Ser Leu Gly Val Thr Thr Phe Thr Arg 340 345 350

Cys Ala Leu Cys Ile Asp Arg Phe Arg Ala Ala Thr Asn Val Gln Met 355 360 365

Tyr Tyr Glu Met Ile Glu Asn Cys Ser Ser Thr Thr Ala Lys Leu Ala 370 375 380

Val Ile Trp Val Gly Ala Leu Leu Leu Ala Leu Pro Glu Val Val Leu 385 390 395 400

Arg Gln Leu Ser Lys Glu Asp Leu Gly Phe Ser Gly Arg Ala Pro Ala 405 410 415

Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr 420 425 430

Val Leu Ala Leu Thr Tyr Asp Ser Ala Arg Leu Trp Trp Tyr Phe Gly
435 440 445

Cys Tyr Phe Cys Leu Pro Thr Leu Phe Thr Ile Thr Cys Ser Leu Val 450 455 460

Thr Ala Arg Lys Ile Arg Lys Ala Glu Lys Ala Cys Thr Arg Gly Asn 465 470 475 480

Lys Arg Gln Ile Gln Leu Glu Ser Gln Met Asn Cys Thr Val Val Ala 485 490 495

Leu Thr Ile Leu Tyr Gly Phe Cys Ile Ile Pro Glu Asn Ile Cys Asn 500 505 510

Ile Val Thr Ala Tyr Met Ala Thr Gly Val Ser Gln Gln Thr Met Asp 515 520 525

Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Cys Val 530 535 540

Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe 545 550 555 560

Met Glu Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser

565 570 575

Thr Val Thr Ser Asp Asp Asp Asp Asp Glu Tyr Thr Thr Glu Leu Glu 580 585 590

Leu Ser Pro Phe Ser Thr Ile Arg Arg Glu Met Ser Thr Phe Ala Ser 595 600 605

Val Gly Thr His Cys 610

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<213> Homo sapiens

<400> 76

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aagtcctatg	tcaccccagt	cctcctttc	tgtctctgca	aacccttcag	tcgggccttc	1680
atggagtgct	gctgctgttg	ctgtgaggaa	tgcattcaga	agtcttcaac	ggtgaccagt	1740
gatgacaatg	acaacgagta	caccacggaa	ctcgaactct	cgcctttcag	taccatacgc	1800
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<210> 77 <211> 613

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 77

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Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro 20 25 30

Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val\$35\$

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg 50 55 60

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe 65 70 75 80

Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro 85 90 95

Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln 115 120 125

Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu 130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly 145 150 155 160

Ile Ser Gly Arg Ser Glu Glu Gln Ser Val Lys Thr Val Pro Gly Ala 165 170 175

Ser Asp Leu Phe Tyr Trp Pro Arg Ala Gly Lys Leu Gln Gly Ser 180 185 190

His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu
195 200 205

Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser 210 215 220

Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser 225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln 245 250 255

Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe $260 \hspace{1cm} 265 \hspace{1cm} 270 \hspace{1cm}$

Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His 275 280 285

Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala 290 295 300

Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe

L

L.

M

His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile 325 330 335

Val Pro Tyr Ile Glu Val Ala Ser Leu Gly Val Thr Thr Phe Thr Leu 340 345 350

Cys Ala Leu Cys Ile Asp Arg Phe Arg Ala Ala Thr Asn Val Gln Met 355 360 365

Tyr Tyr Glu Met Ile Glu Asn Cys Ser Ser Thr Thr Ala Lys Leu Ala 370 375 380

Val Ile Trp Val Gly Ala Leu Leu Leu Ala Leu Pro Glu Val Val Leu 385 390 395 400

Arg Gln Leu Ser Lys Glu Asp Leu Gly Phe Ser Gly Arg Ala Pro Ala 405 410 415

Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr 420 425 430

Val Leu Ala Leu Thr Tyr Asp Ser Ala Arg Leu Trp Trp Tyr Phe Gly 435 440 445

Cys Tyr Phe Cys Leu Pro Thr Leu Phe Thr Ile Thr Cys Ser Leu Val 450 460

Thr Ala Arg Lys Ile Arg Lys Ala Glu Lys Ala Cys Thr Arg Gly Asn 470 475 480

Lys Arg Gln Ile Gln Leu Glu Ser Gln Met Asn Cys Thr Val Val Ala 485 490 495

Leu Thr Ile Leu Tyr Gly Phe Cys Ile Ile Pro Glu Asn Ile Cys Asn 500 505 510

Ile Val Thr Ala Tyr Met Ala Thr Gly Val Ser Gln Gln Thr Met Asp 515 520 525

Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Tyr Val 530 540

Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe 545 550 555 560

Met Glu Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser 565 570 575

Thr Val Thr Ser Asp Asp Asp Asp Asp Glu Tyr Thr Thr Glu Leu Glu 580 585 590

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Val Gly Thr His Cys 610

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<220>

<223> Novel Sequence

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ttcatcacca	tcctcctcat	cctgatccag	aacttcaagc	aagacctggt	catctggccg	900
tccctcttct	tctgggtggt	ggccttcaca	tttgctaatt	cagccctaaa	ccccatcctc	960
tacaacatga	cactgtgcag	gaatgagtgg	aagaaaattt	tttgctgctt	ctggttccca	1020
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<210> 79

<211> 361

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 79

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser 1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys 20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val 35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu 50 55 60

Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn 65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu 85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His $100 \hspace{1.5cm} 105 \hspace{1.5cm} 105$

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr 115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Glu 130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser Phe Phe Ile Met Trp Ser Pro Ile Phe Ile Thr Ile Leu Leu Ile Leu Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys

Arg Asn Asp Leu Ser Ile Ile Ser Gly

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       DNA
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                                                                     120
gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc
                                                                     180
gccctggtgc tggtggcgcg ccgacgacgc cgcggcgcga ctgcctgcct ggtactcaac
                                                                     240
ctcttctgcg cggacctgct cttcatcagc gctatccctc tggtgctggc cgtqcqctgq
                                                                     300
actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgaccctg
                                                                     360
agcggcagcg tcaccatcct cacgetggcc gcggtcagcc tgaatcgcat ggtgtgcatc
                                                                     420
gtgcacctgc agcgcggcgt gcggggtcct gggcggcqqq cqcqqqcaqt qctqctqqcq
                                                                     480
ctcatctggg gctattcggc ggtcgccgct ctgcctctct gcgtcttctt tcgagtcgtc
                                                                     540
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                                                                     600
attectggag agatetegtg ggatgtetet titgttaett tgaacttett ggtgecagga.
                                                                     660
ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg
                                                                     720
ctcacggtaa gcctggccta ctcggagagc caccagatcc gcgtgtccca gcaggacttc
                                                                     780
eggetettee geaccetett cetecteatg gteteettet teateatgtg gagececate
                                                                     840
atcatcacca tectecteat eetgateeag aactteaage aagacetggt catetggeeg
                                                                     900
tecetettet tetgggtggt ggeetteaea tttgetaatt cageectaaa ceceateete
                                                                     960
tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca
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<210> 81 <211> 361 <212> PRT

<213> Unknown

<220>

<223> Novel Sequence

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- Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys 20 25 30
- Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val 35 40 45
- Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu 50 55 60
- Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn 65 70 75 80
- Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu 85 90 95
- Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His 100 105 110
- Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr 115 120 125
- Leu Ala Ala Val Ser Leu Asn Arg Met Val Cys Ile Val His Leu Gln 130 135
- Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala 145 150 155 160
- Leu Ile Trp Gly Tyr Ser Ala Val Ala Leu Pro Leu Cys Val Phe \$165\$ \$170\$ \$175\$
- Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser 180 185 190
- Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp 195 200 205
- Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val 210 215 220

Ile 225	Ser	Tyr	Ser	Lys	Ile 230	Leu	Gln	Ile	Thr	Lys 235	Ala	Ser	Arg	Lys	Arg 240	
Leu	Thr	Val	Ser	Leu 245	Ala	Tyr	Ser	Glu	Ser 250	His	Gln	Ile	Arg	Val 255	Ser	
Gln	Gln	Asp	Phe 260	Arg	Leu	Phe	Arg	Thr 265	Leu	Phe	Leu	Leu	Met 270	Val	Ser	
Phe	Phe	Ile 275	Met	Trp	Ser	Pro	Ile 280	Ile	Ile	Thr	Ile	Leu 285	Leu	Ile	Leu	
Ile	Gln 290	Asn	Phe	Lys	Gln	Asp 295	Leu	Val	Ile	Trp	Pro 300	Ser	Leu	Phe	Phe	
Trp 305	Val	Val	Ala	Phe	Thr 310	Phe	Ala	Asn	Ser	Ala 315	Leu	Asn	Pro	Ile	Leu 320	
Tyr	Asn	Met	Thr	Leu 325	Cys	Arg	Asn	Glu	Trp 330	Lys	Lys	Ile	Phe	Cys 335	Cys	
Phe	Trp	Phe	Pro 340	Glu	Lys	Gly	Ala	Ile 345	Leu	Thr	Asp	Thr	Ser 350	Val	Lys	
Arg	Asn	Asp 355	Leu	Ser	Ile	Ile	Ser 360	Gly								
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<220 <223		Novel	l Sed	quenc	ce											
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tgtg	cca	cat a	acct	gctga	at ct	tcgt	ggt	g ggd	eget	gtgg	gcaa	atgg	gct (gacct	gtctg	180
gtca	tcct	iga q	gcca	caag	ge ca	atgc	gcaco	g cct	tacca	aact	acta	acct	ett (cagc	ctggcc	240
gtgt	cgga	acc t	tgct	ggtg	ct go	ctggt	gggd	c ct	gaaa	ctgg	agct	ctat	tga (gatgt	ggcac	300
aact	acco	act t	teete	acta	מת כי	rtta	ataaa	r taa	~tatt	tcc	acad	aact:	act (~+++/	racato	360

gtctgcct	gg cctcagtgct	caacgtcact	gccctgagcg	tggaacgcta	tgtggccgtg	420
gtgcaccc	ac tccaggccag	gtccatggtg	acgcgggccc	atgtgcgccg	agtgcttggg	480
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ccacgggc	cc tctacaacat	ggtagtgcag	accaccgcgc	tgctcttctt	ctgcctgccc	660
atggccat	ca tgagcgtgct	ctacctgctc	attgggctgc	gactgcggcg	ggagaggctg	720
ctgctcat	gc aggaggccaa	gggcaggggc	tctgcagcag	ccaggtccag	atacacctgc	780
aggctcca	gc agcacgatcg	gggccggaga	caagtgaaaa	agatgctgtt	tgtcctggtc	840
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cacagete	cc acagecteag	caggatgacc	acaggcagca	ccctgtgtga	tgtgggctcc	1140
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<211> 403

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 83

Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln 20 25 30

Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe 35 40 45

Val Val Gly Ala Val Gly As
n Gly Leu Thr Cys Leu Val Ile Leu Arg $50 \hspace{1.5cm} 55 \hspace{1.5cm} 60 \hspace{1.5cm}$

His 65	Lys	Ala	Met	Arg	Thr 70	Pro	Thr	Asn	Tyr	Tyr 75	Leu	Phe	Ser	Leu	Ala 80
Val	Ser	Asp	Leu	Leu 85	Val	Leu	Leu	Val	Gly 90	Leu	Pro	Leu	Glu	Leu 95	Tyr
Glu	Met	Trp	His 100	Asn	Tyr	Pro	Phe	Leu 105	Leu	Gly	Val	Gly	Gly 110	Cys	Tyr
Phe	Arg	Thr 115	Leu	Leu	Phe	Glu	Met 120	Val	Cys	Leu	Ala	Ser 125	Val	Leu	Asn
Val	Thr 130	Ala	Leu	Ser	Val	Glu 135	Arg	Tyr	Val	Ala	Val 140	Val	His	Pro	Leu
Gln 145	Ala	Arg	Ser	Met	Val 150	Thr	Arg	Ala	His	Val 155	Arg	Arg	Val	Leu	Gly 160
Ala	Val	Trp	Gly	Leu 165	Ala	Met	Leu	Cys	Ser 170	Leu	Pro	Asn	Thr	Ser 175	Leu
His	Gly	Ile	Arg 180	Gln	Leu	His	Val	Pro 185	Cys	Arg	Gly	Pro	Val 190	Pro	Asp
Ser	Ala	Val 195	Cys	Met	Leu	Val	Arg 200	Pro	Arg	Ala	Leu	Tyr 205	Asn	Met	Val
Val	Gln 210	Thr	Thr	Ala	Leu	Leu 215	Phe	Phe	Cys	Leu	Pro 220	Met	Ala	Ile	Met
Ser 225	Val	Leu	Tyr	Leu	Leu 230		Gly		-	Leu 235	_	Arg	Glu	Arg	Leu 240
Leu	Leu	Met	Gln	Glu 245	Ala	Lys	Gly	Arg	Gly 250	Ser	Ala	Ala	Ala	Arg 255	Ser
Arg	Tyr	Thr	Cys 260	Arg	Leu	Gln	Gln	His 265	Asp	Arg	Gly	Arg	Arg 270	Gln	Val

Lys Lys Met Leu Phe Val Leu Val Val Val Phe Gly Ile Cys Trp Ala

Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr 290 295 300	
Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile 305 310 315 320	
Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met 325 330 335	
Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala 340 345 350	
Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg 355 360 365	
Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp 370 375 380	
Val His Pro Leu Ala Gly Asn Asp Gly Pro Glu Ala Gln Gln Glu Thr 385 390 395 400	
Asp Pro Ser	
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gcgctctggg tgttctgctg ccgcatgcag cagtggacgg agacccgcat ctacatgacc	180
aacctggcgg tggccgacct ctgcctgctg tgcaccttgc ccttcgtgct gcactccctg	240
cgagacacct cagacacgcc gctgtgccag ctctcccagg gcatctacct gaccaacagg	300
tacatgagca tcagcctggt cacggccatc gccgtggacc gctatgtggc cgtgcggcac	360
cegetgegtg ecegeggget geggteeeee aggeaggetg eggeegtgtg egeggteete	420

480

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ttctgcttca ggagcacccg gcacaatttc aactccatgc ggttcccgct gctgggattc 540 tacctgcccc tggccgtggt ggtcttctgc tccctgaagg tggtgactgc cctggcccag 600 aggecaceca cegacgtggg geaggeagag gecaceegea aggetaaaeg catggtetgg 660 gccaacctcc tggtgttcgt ggtctgcttc ctgcccctgc acgtggggct gacagtgcgc 720 ctcgcagtgg gctggaacgc ctgtgccctc ctggagacga tccgtcgcgc cctgtacata 780 accaqcaaqc teteagatge caactgetge etggacgeca tetgetacta etacatggee 840 aaggagttee aggaggegte tgeactggee gtggeteece gtgetaagge ceacaaaage 900 930 caggactete tgtgcgtgac cetegeetaa

<210> 85

<211> 309

<212> PRT

<213> Unknown

<220>

<223> Novel Sequence

<400> 85

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro 1 5 10 15

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val 20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg 35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val 50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu 65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr 85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val 100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg 115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val 130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly 145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro 165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Phe Cys Ser Leu 180 185 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln 195 200 205

Ala Glu Ala Thr Arg Lys Ala Lys Arg Met Val Trp Ala Asn Leu Leu 210 215 220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg 225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg 245 250 255

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp 260 265 270

Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala 275 280 285

Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu 290 295 300

Cys Val Thr Leu Ala 305

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<212> DNA

<213> Unknown

<220>

<223> Novel Sequence

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cagageegat ecaagagggg caeegaggat gaggaggeea agggegtgea geagtatgtg	180
cctgaggagt gggcggagta cccccggccc attcaccctg ctggcctgca gccaaccaag	240
cccttggtgg ccaccagece taaccccgae aaggatgggg gcaccccaga cagtgggcag	300
gaactgaggg gcaatctgac aggggcacca gggcagaggc tacagatcca gaaccccctg	360
tatccggtga ccgagagctc ctacagtgcc tatgccatca tgcttctggc gctggtggtg	420
tttgcggtgg gcattgtggg caacctgtcg gtcatgtgca tcgtgtggca cagctactac	480
ctgaagagcg cctggaactc catccttgcc agcctggccc tctgggattt tctggtcctc	540
tttttctgcc tccctattgt catcttcaac gagatcacca agcagaggct actgggtgac	600
gtttettgte gtgeegtgee etteatggag gteteetete tgggagteae gaettteage	660
ctctgtgccc tgggcattga ccgcttccac gtggccacca gcaccctgcc caaggtgagg	720
cccatcgagc ggtgccaatc catcctggcc aagttggctg tcatctgggt gggctccatg	780
acgctggctg tgcctgagct cctgctgtgg cagctggcac aggagcctgc ccccaccatg	840
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ctggtgatga cctaccagaa cgcccgcatg tggtggtact ttggctgcta cttctgcctg	960
cccatcctct tcacagtcac ctgccagetg gtgacatggc gggtgcgagg ccctccaggg	1020
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aaccagttct ccaccttctt caagggcgcc atcaccccag tgctgctcct ttgcatctgc	1260
aggeegetgg geeaggeett eetggaetge tgetgetget getgetgtga ggagtgegge	1320
ggggettegg aggeetetge tgeeaatggg teggaeaaca ageteaagae egaggtgtee	1380
tettecatet aettecaeaa geeeagggag teaeceecae teetgeeeet gggeaeacet	1440
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<210> 87 <211> 481 <212> PRT <213> Unknown

<220>

<223> Novel Sequence

<400> 87

Met Arg Trp Leu Trp Pro Leu Ala Val Ser Leu Ala Val Ile Leu Ala 1 5 10 15

Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg 20 25 30

His Arg Ala Glu Thr Glu Glu Gln Ser Arg Ser Lys Arg Gly Thr 35 40 45

Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp 50 60

Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys 65 70 75 80

Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro 85 90 95

Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln $100 \,$ $105 \,$ $110 \,$

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr 115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly 130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr 145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp 165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe As
n Glu Ile 180 \$185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe 195 200 205 Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu 210 215 220

Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg 225 230 235 240

Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp 245 250 255

Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Leu Trp Gln Leu 260 265 270

Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met 275 280 285

Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr 290 295 300

Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu 305 310 315 320

Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg 325 330 335

Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln 340 345 350

Cys Glu Ser Gln Leu Lys Ser Thr Val Val Gly Leu Thr Val Val Tyr 355 360 365

Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr 370 375 380

Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile 385 390 395 400

Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu 405 410 415

Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys 420 425 430

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Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala
Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr
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Cys
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Asp Cys Gly Leu Phe
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<210> 93
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Asp Cys Gly Leu Phe
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<220> <223> Novel Sequence

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<223> Novel Sequence

Met Gly Cys Leu Gly Asn Ser Lys Thr Glu Asp Gln Arg Asn Glu Glu

<210> 96 <211> 393

<212> PRT

<213> Unknown

<220>

<400> 96

M

Lys Ala Gl
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n Leu Gl
n Lys 20 $$ 25 $$ 30

Asp Lys Gln Val Tyr Arg Ala Thr His Arg Leu Leu Leu Gly Ala 35 40 45

Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His 50 55 60

Val Asn Gly Phe Asn Gly Glu Gly Glu Glu Asp Pro Gln Ala Ala 65 70 75 80

Arg Ser Asn Ser Asp Gly Glu Lys Ala Thr Lys Val Gln Asp Ile Lys 85 90 95

Asn Asn Leu Lys Glu Ala Ile Glu Thr Ile Val Ala Ala Ser Asn Leu 100 105 110

Val Pro Pro Val Glu Leu Ala Asn Pro Glu Asn Gln Phe Arg Val Asp 115 120 125

Tyr Ile Leu Ser Val Met Asn Val Pro Asn Phe Asp Phe Pro Pro Glu 130 135 140

Phe Tyr Glu His Ala Lys Ala Leu Trp Glu Asp Glu Gly Val Arg Ala 145 150 155 160

Cys Tyr Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln Tyr 165 170 175

Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val Pro Ser 180 185 190

Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe Glu
195 200 205

Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val Gly 210 215 220

Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp Val 225 230 235 240

Thr	Ala	Ile	Ile	Phe 245	Val	Val	Ala	Ser	Ser 250	Ser	Tyr	Asn	Met	Val 255	Ile
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Lys	Ser	Ile 275	Trp	Asn	Asn	Arg	Trp 280	Leu	Arg	Thr	Ile	Ser 285	Val	Ile	Leu
Phe	Leu 290	Asn	Lys	Gln	Asp	Leu 295	Leu	Ala	Glu	Lys	Val 300	Leu	Ala	Gly	Lys
Ser 305	Lys	Ile	Glu	Asp	Tyr 310	Phe	Pro	Glu	Phe	Ala 315	Arg	Tyr	Thr	Thr	Pro 320
Glu	Asp	Ala	Thr	Pro 325	Glu	Pro	Gly	Glu	Asp 330	Pro	Arg	Val	Thr	Arg 335	Ala
Lys	Tyr	Phe	Ile 340		Asp	Glu	Phe	Leu 345	Arg	Ile	Ser	Thr	Ala 350	Ser	Gly
Asp	Gly	Arg 355	His	Туг	Cys	Tyr	Pro 360		Phe	Thr	Cys	Ala 365		Asp	Thr
Glu	Asn 370		Arg	Arg	Val	Phe 375		Asp	Cys	Arg	Asp 380		: Ile	Gln	Arg
Met 385		Leu	Arg	, Asp	Cys 390		Leu	ı Phe	:						
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180

240

300

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Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu 50 55 60

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Ser Tyr Arg Ala Lys Met Pro Pro Pro Arg Cys Ala Leu Ile Leu Ala 115 120 125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Leu Ala Leu 130 $$135\$

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser 145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe $165 \,$ $170 \,$ $175 \,$

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr 180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val 195 200 205

Ile Thr Met Gln Thr Leu Val Leu Val Asp Leu His Pro Ser Val 210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr 225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly
260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala 275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser 290 295 300

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